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Citation for the original published paper (version of record):

Lundh, T. (2000). In search of an evolutionary coding style. Stony Brook IMS Preprint, 00(03)

N.B. When citing this work, cite the original published paper.

In search of an evolutionary coding style

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Keywords: style, code, evolution, artificial life, emergence, complexity, DNA, Avida, stylometry, GRASP, Halstead's complexity.

Abstract

In the near future, all the human genes will be identified. But understanding the functions coded in the genes is a much harder problem. For example, by using block entropy, one has that the DNA code is closer to a random code than written text, which in turn is less ordered than an ordinary computer code; see [17].

Instead of saying that the DNA is badly written, using our programming standards, we might say that it is written in a different style — an evolutionary style.

We will suggest a way to search for such a style in a quantified manner by using an artificial life program, and by giving a definition of general codes and a definition of style for such codes.

1 Background

Let us as a background cite three different sources.

The first is J. Madox's comment on page 376 in [11].

"In genetics for example, the task of understanding the functions of all the 100,000 human genes will require a much greater effort than that involved in their identification, and by a factor 10 or more."

Chris Adami from Caltech made, in his survey talk at Renaissance Technologies in Stony Brook 10/27/98 about artificial life, a brief remark about the quality

of the evolved program codes in his avida set up. He said something like this:

"The codes that are evolved will eventually be almost totally unreadable. Things are never used only once, but two or more times. It is a kind of a 'madman's' code."

In recent years, a lot of examples have been found where genes have been "reused" for different purposes during development. As an example, take the *runt* gene in *Drosophila*, which is used in sex determination, segmentation and central nervous system creation. In [7] the authors write:

"As mature organisms we are composed of an astonishing array of diverse cell types—all derived from a single-celled zygote. When faced with the task of generating such cellular diversity in a reproducible fashion, how has the embryo chosen to respond? Recent work in a number of developmental systems has suggested that the embryo has employed two approaches. First, given finite resources, the embryo has efficiently chosen to reutilize a limited set of proteins in different temporal and spatial contexts to create cellular diversity. Second, the embryo has also chosen to install molecular redundancies to ensure the reproducibility of these patterns from individual to individual."

How can we capture these comments about the style or quality of the computer code and the DNA, in a quantified manner? Can we do that in such a general manner that we will be able to use analogous quality measure both for carbon- and silicon based genetic codes?

1.1 Plan of the paper

We give a straightforward but general definition of a "code", a general definition of the "style" of such

*This work was done at SUNY Stony Brook under the support (408003356-8) from the Swedish Natural Science Research Council, NFR.

codes using a given set of measures. We will also suggest such measures of characteristic features, such as some type of “madness”, the robustness, and the amount of reuse, of such codes. Finally, we will make some “baby-experiments” by running the avida program and analyze samples of the evolved code, generate two simulated programs in the same function class, and eventually stylistically compare the real evolved code with these simulated codes, all of this will be done in a C++ program. Some results will be graphically displayed at the end.

1.2 Future goals

One could then more systematically run the avida program (or something similar) and analyze the evolved codes stylistically with more realistic, and a higher number of comparison codes. By changing parameters for the set up in avida, one might eventually capture some common features. By comparing the carbon based programming style and the silicon based style, it might be possible to find some common parts that would describe the natural programming style for evolution. That would in turn help us read carbon based code. And it would also give us some hints how to create more robust computer programs, by looking at how nature has solved such problems.

1.3 Questions

Is there an existing way to study the style or quality of the DNA? And is there any existing theory in the information sciences that deals with this on the silicon side? We are aiming at a complexity level higher than the usual information theory measures, such as the notion of entropy (see the comment in Section 6.2).

1.4 Acknowledgement

I would very much like to thank professor G. Thomsen for listen to my ideas and for his constant encouragement. I would also like to thank him for making me feel so much at home in his *Xenopus* lab, and teaching me the basics in frog handling and cultural behaviour in the life sciences.

I would also like to thank Dr D. Slice for his interest and all his help and suggestions.

B. Cohen has been a good source for me concerning the existing computer code complexity measures. He has also been a fruitful discussion partner.

I am grateful to S. Sutherland for reading an earlier version of this paper and giving me useful comments and pointing out errors and weaknesses.

Finally I would like to thank D. Brander for playing squash with me and for trying to teach me some grammar. (All the remaining language errors are naturally completely my own fault.)

2 A general code

We will give a general definition of a code as a string of generalized “letters” from a given alphabet, that when interpreted, will define a function. This interpretation is not unique, i.e. many different codes will produce the same function. That fact will give us a way to study classes of codes. That is, two codes are in the same class if their interpretation gives equivalent functions.

2.1 Codes

We will give a definition of a code by using an underlying *alphabet*, and a generalized *interpreter*.

Definition 2.1 *Let us define a **code** to be a finite string of “letters” taken from an “alphabet”, \mathcal{A} ,*

$$\text{Code} = \{\alpha_i\}_{i=1}^k, \text{ where } \alpha_i \in \mathcal{A},$$

such that when the code is interpreted, the code will represent a well defined function (or a process), $\text{Code}_j \rightarrow f_j$, with a domain D_{f_j} such that for all inputs, $x \in D_{f_j}$, to the interpretation of the code, will give $f_j(x)$ as the output¹.

2.2 Classes of codes

From the above definition of codes, we see that different codes can have the same function representation, see Example 2.5 below.

Let us therefore introduce the following classification. Let the code Code_f and the codes Code_{f_i} have the functions f and f_i as their representations.

Definition 2.2 *Let the code class with respect to the function f be the following (infinite) set of codes.*

$$\mathcal{C}_f = \{\text{Code}_{f_i} : f_i(x) = f(x), \text{ for all } x \in D_f\}.$$

Remark 2.3 *If the interpreter is not able to produce a well defined function from the code Code , we say that Code is in the error class \mathcal{C}_ϵ . That (huge) class can be viewed as the complement to all interpretable codes.*

¹Note that we here consider a function in a general sense, i.e. not necessarily numerical.

Question 2.4 *With the suggested norm of \mathcal{C}_f below, is \mathcal{C}_f compact? Do there exist extremal codes?*

Example 2.5 *Let*

$$f(x) = \frac{1}{x-2},$$

$$g(x) = \begin{cases} \frac{x+2}{x^2-4} & \text{if } x \neq -2 \\ -\frac{1}{4} & \text{if } x = -2 \end{cases}$$

and

$$h(x) = \begin{cases} -\frac{1}{4} & \text{if } x = -2 \\ -\frac{1}{2} & \text{if } x = 0 \\ -1 & \text{if } x = 1 \\ 1 & \text{if } x = 3 \\ \frac{1}{2} & \text{if } x = 4 \end{cases}$$

Note that Code_g and Code_f are both in \mathcal{C}_h ; and $\mathcal{C}_f = \mathcal{C}_g \subset \mathcal{C}_h$.

Remark 2.6 *One common way to view functions is as black boxes. Here we are interested of the internal structure of such black boxes performing equivalent tasks.*

3 The style of a code

We will now give a description of a method to characterize different coding styles. Since different codes do not differ in function in the same class, we say that they differ in *style*. How can we characterize such style?

Given a set of measures on the codes, we propose a way to characterize style of a subset of codes in the code class as an extremal unit weight vector that will act as a stylistic “fingerprint”. We will also give an algorithm for “stylistic translations”, and an index which reveals how well a given subset represents a common style.

The methods we use apply very elementary mathematics, and maybe even more basic statistical methods. That will hopefully make it accessible to a wide scientific audience who are interested in “style”.

3.1 A measure on \mathcal{C}_f

Let us now study measures on \mathcal{C}_f . Let

$$\mu_i : \mathcal{C}_f \rightarrow [0, 1].$$

Let us consider the following profile measure

$$\boldsymbol{\mu} = (\mu_1, \mu_2, \dots, \mu_n)$$

of codes in \mathcal{C}_f . If a given measure has a range outside $[0, 1]$, let us use the transformation

$$x \rightarrow \frac{x}{1+x}$$

to make it fit into $[0, 1]$.

We define the following scalar measure.

$$\nu_{\mathbf{w}}(\text{Code}_g) = \mathbf{w} \cdot \boldsymbol{\mu}(\text{Code}_g),$$

where \mathbf{w} is a normalized weight vector such that $\|\mathbf{w}\| = 1$, for some norm $\|\cdot\|$. For example, let

$$\|\mathbf{w}\| = \|\mathbf{w}\|_p = \left(\sum_{i=1}^n |w_i|^p \right)^{\frac{1}{p}},$$

where $p \geq 1$. As a default norm, let us use $\|\cdot\| = \|\cdot\|_2$.

3.2 Extremal weights

Let us use the above measure to try to capture a characterization of “style” of codes.

Suppose that we have two sample sets, A and B , of codes in \mathcal{C}_f . We will try to find a style characterization of the codes in A relative to B .

We can think of A as the set of codes we are stylistically interested in and B as a complementary environment.

Let us define a vector $\mathbf{u} = (u_1, u_2, \dots, u_n)$ in the following way.

$$\mathbf{u} = \sum_{a_i \in A} \sum_{b_j \in B} (\boldsymbol{\mu}(a_i) - \boldsymbol{\mu}(b_j)). \quad (1)$$

Let us now normalize \mathbf{u} to a unit vector.

$$\mathbf{w}^+ = \mathbf{w}^+(A) = \frac{\mathbf{u}}{\|\mathbf{u}\|}. \quad (2)$$

Let us now study the random variable

$$X = \nu_{\mathbf{w}}(a_i) - \nu_{\mathbf{w}}(b_j), \quad (3)$$

where a_i is a randomly chosen code in A , with uniform probability², and b_j is randomly chosen in B . Note that X is dependent on the chosen \mathbf{w} .

Proposition 3.1 *Let X be the random variable defined in (3) and let \mathbf{w}^+ be the unit vector from (2). Then we have that picking $\mathbf{w} = \mathbf{w}^+$ will maximize the expected value of X , $E(X)$.*

²The probability to choose a_i is $1/\#(A)$.

Proof: Let $\#(\cdot)$ denote the cardinality of a set and let $M = \#(A)\#(B)$. The expectation for a general weight vector \mathbf{w} will be easily computed.

$$\begin{aligned} E(X) &= \frac{1}{M} \sum_{a_i \in A} \sum_{b_j \in B} (\nu_{\mathbf{w}}(a_i) - \nu_{\mathbf{w}}(b_j)) = \\ &= \frac{1}{M} \sum_{a_i \in A} \sum_{b_j \in B} (\mathbf{w} \cdot \boldsymbol{\mu}(a_i) - \mathbf{w} \cdot \boldsymbol{\mu}(b_j)) = \frac{\mathbf{w} \cdot \mathbf{u}}{M}. \end{aligned}$$

Since $\|\mathbf{w}\| = 1$ we have that

$$|E(X)| \leq \frac{\|\mathbf{u}\|}{M}.$$

Let us now look at the special case $\mathbf{w} = \mathbf{w}^+$. We have then that

$$\begin{aligned} E(X) &= \frac{\mathbf{w}^+ \cdot \mathbf{u}}{M} = \frac{1}{M} \frac{\mathbf{u}}{\|\mathbf{u}\|} \cdot \mathbf{u} = \\ &= \frac{\|\mathbf{u}\|^2}{M\|\mathbf{u}\|} = \frac{\|\mathbf{u}\|}{M}. \end{aligned}$$

Thus we see that taking \mathbf{w} to be \mathbf{w}^+ will maximize $E(X)$. \square

3.3 A fingerprint on the hyper sphere

We can now view the unit vector $\mathbf{w}^+(A) = \mathbf{w}^+$ on the unit hyper³ sphere as a “fingerprint” of the style of codes in A relative to B with respect to the list of given measures in $\boldsymbol{\mu}$.

Remark 3.2 *If there is a superset of codes $B_1 \supset B$ which is enough separated, then the fingerprint \mathbf{w}^+ of A relative to B_1 can be expected to be a more refined characterization of the “style” in A than the \mathbf{w}^+ of A relative to B .*

3.4 A universal character

One would hope that similar classes, \mathcal{C}_f , would give similar fingerprints \mathbf{w}^+ for different function codes created by the same code writing agent.

3.5 Stability with respect to the vector $\boldsymbol{\mu}$

There is a stability feature built into \mathbf{w}^+ in the sense that if you would like to find a stylistic quality in a group of codes, you try to find “relevant” measures in the vector $\boldsymbol{\mu}$. What happens if, in addition to your relevant measures, you also take a sequence of

irrelevant measures (where, for example, the codes look more or less randomly distributed, or even just the same)? If the environment, i.e. B , is rich enough, then your profile will just be about zero at the tail, where the non-relevant measures are. That means you don’t have to be restrictive when you pick your measures — if some happen to be worthless, that will be taken care of by itself.

3.6 Is there a common style in A ?

Given two subsets, A and B in \mathcal{C}_f , of codes, we have now a method for finding a common style in A , in relation to B , as a unit vector $\mathbf{w}^+(A)$. (As a special case, we can let B be the complement of A in \mathcal{C}_f . Then we can talk about *the* style of A .)

This process can be executed even if A and B are just randomly chosen subsets in \mathcal{C}_f where we can not expect to find any stylistic common features in A in comparison to all the codes in B . How can we find out if A really has a common style, in comparison to B , that can be captured by the chosen measure profile $\boldsymbol{\mu}$?

Let us go back to Equation (3) and the random variable X . Let us also define a similar s.v. Y such that

$$Y = \nu_{\mathbf{w}}(c_i) - \nu_{\mathbf{w}}(c_j),$$

where c_i and c_j are randomly chosen, with equal probability, in $A \cup B$. Note that the underlying \mathbf{w} is $\mathbf{w}^+(A)$. From Proposition 3.1 above, the expected value of X will then be maximal. Let us denote that value by m , i.e. let $E(X) = m$. From the proof of Proposition 3.1 we see that

$$m = \frac{\|\mathbf{u}\|}{\#A\#B}.$$

Hence, loosely speaking, m is large if A has a characteristic style that is captured by the measure profile $\boldsymbol{\mu}$. How large can m get? Or in other words: how large can $\|\mathbf{u}\|$ get? Since all the measures $\mu_k(\cdot)$ are bounded above by 1 and below by 0 we have that a component u_i of the \mathbf{u} vector is also bounded.

$$\begin{aligned} u_k &= \sum_{a_i \in A} \sum_{b_j \in B} (\mu_k(a_i) - \mu_k(b_j)) \leq \\ &\leq \sum_{a_i \in A} \sum_{b_j \in B} (1 - 0) = \#A\#B = M. \end{aligned}$$

If we are using the standard norm $\|\cdot\| = \|\cdot\|_2$, we get that $\|\mathbf{u}\| \leq \sqrt{n}M$ and hence $\|\mathbf{u}\| \leq \sqrt{n}M$.

Let us normalize m to get the following index

$$\theta = \frac{m}{\sqrt{n}}.$$

³if $n > 3$

We see that $\theta \in [0, 1]$ and it will be closer to 1 when the fingerprint is good.

On the other hand, due to the Remark 3.3 below, we might also need an invariant index.

Let us use the variances of the random variables X, Y in the following way. Let

$$\sigma_A^2 = E((X - m)^2), \text{ and let } \sigma_{AB}^2 = E(Y^2).$$

Note that we immediately have that $E(Y) = 0$. Let us suggest an index η of how well the measure profile μ can capture a common style, if it exists at all, in A in comparison to the codes in B . Let

$$\eta = \eta(A, B, \mu) = \frac{\sigma_{AB}^2}{\sigma_A^2} = \frac{E(Y^2)}{E(X^2) - m^2}. \quad (4)$$

Remark 3.3 *Note that if all the measures in μ are multiplied by a factor $k < 1$, i.e. $\mu_i \rightarrow k\mu_i$, then $m \rightarrow km$, $\sigma_A^2 \rightarrow k^2\sigma_A^2$, and $\sigma_{AB}^2 \rightarrow k^2\sigma_{AB}^2$. Hence η would not change, but $\theta \rightarrow k\theta$.*

3.6.1 Principal component analysis

A very illustrative, and very popular, technique when looking for connections in a multidimensional environment is the *principal component analysis*. It is a two dimensional diagram with coordinate axis the two eigenvectors with the largest eigenvalues of the covariance matrix \mathcal{M} . Let $C = A \cup B$ and let $N = \#C$. We denote the codes in C by c_j , then

$$\mathcal{M}_{i,j} = \text{Cov}\left((\mu_i(c_1), \mu_i(c_2), \dots, \mu_i(c_N)), (\mu_j(c_1), \mu_j(c_2), \dots, \mu_j(c_N))\right).$$

For more details, see any book in multivariate analysis, for example [13].

If in such a diagram, the codes A we are interested in are clearly separated from the B codes, then we could say that there is a common style in A , and if that is the case and if the largest eigenvalue is considerably larger than the second one, then the fingerprint \mathbf{w} and the first eigenvector should be close to each other. That is indeed the case in Figure 7.

3.6.2 Cluster analysis

Another tool from the multivariate toolbox could be used to study the question about a common style in A . This method is based on an iteration fusion of close points until the desired number of subsets are obtained. To measure the closeness, we might pick our scalar measure $\nu_{\mathbf{w}^+}$.

In order to check if there is a common style in A , we can ask how well the points in A are clustered.

3.7 Style translations by iterations

Using the above construction, let us here indicate an algorithm how to “stylistically translate” a code a in $A \subset \mathcal{C}_f$, into the style in $B \subset \mathcal{C}_f$.

1. Compute

$$\mathbf{v} = \sum_{b_i \in B} (\mu(b_i) - \mu(a)).$$

2. Find the dominating component of the vector \mathbf{v} , i.e. let

$$v_m = \max_{1 \leq i \leq n} |v_i|.$$

3. Study the measure μ_m and stylistically rewrite a such that $\mu_m(a)$ would increase approximately v_m units (decrease if $v_m < 0$).
4. Iterate the process until sufficient accuracy is attained. The accuracy is measured by $\|\mathbf{v}\|$.

Suppose the final accuracy is δ and denote the rewritten a by a' . Let $\mathbf{w} = \mathbf{w}^+(B)$ and let Z be the random variable

$$Z = \nu_{\mathbf{w}}(b_i) - \nu_{\mathbf{w}}(a'),$$

for a randomly chosen b_i in B . Now the expected value of Z will be

$$E(Z) = \frac{\sum_{i \in B} \mathbf{w} \cdot (\mu(b_i) - \mu(a'))}{\#(B)},$$

where $\#(\cdot)$ stands for the number of elements in the set. That is

$$E(Z) = \frac{\mathbf{w} \cdot \mathbf{v}}{\#(B)}.$$

Now if we have the norm $\|\cdot\|$ as the default $\|\cdot\|_2$ we can use Cauchy–Schwarz’ inequality to get that

$$|E(Z)| \leq \frac{\delta}{\#(B)}.$$

In other words, the fingerprint \mathbf{w}^+ of B would hardly “feel” the difference between a' and the codes in B if δ is small.

4 Different levels of Code

So far we have just been studying a code on a singular level. In this section we will describe a way to separate the codes into different levels. One could then ask questions about the styles on different levels. Are the styles similar even on different levels, etc?

We will view a code as a composition of lower level codes. Let us use the definition of emergence given in [4] on p. 518.

P is an emergent property of S^2

\iff

$$P \in \text{Obs}^2(S^2), \text{ but } P \notin \text{Obs}^2(S_{i_1}^1) \quad \forall i_1.$$

Let us explain this more in detail, and similarly display a concrete example of a computer code, where the inputs are integers.

In this case, let S^0 be input values, e.g. $S_i^0 \in \mathbb{N}$, and let $\{\text{Int}^i\}_{i=0}^n$ be a given sequence of sets of interactions, e.g. $\text{Int}^0 = \{+, -\}$, $\text{Int}^1 = \{*, \div\} \cup \text{Int}^0$, $\text{Int}^2 = \{=, <, >\} \cup \text{Int}^1$, etc. Let $\{\text{Obs}^i\}_{i=0}^n$ be the related observational function, e.g. $\text{Obs}^0(x) = \text{value of } x \text{ as an integer}$, $\text{Obs}^2(x > y) = \text{true or false}$.

From the given sequences $\{\text{Int}^i\}_{i=0}^n$ and $\{\text{Obs}^i\}_{i=0}^n$ we get the higher order structures as a “reaction”, R , in the following manner.

$$S^1 = R(S^0, \text{Obs}^0, \text{Int}^0),$$

$$S^2 = R(S^1, \text{Obs}^1, \text{Int}^1),$$

see [4] for details.

We have then that in our example, -1 is an emergent property of $S^1 = \mathbf{Z}$, $1/2$ is an emergent property of $S^2 = \mathbf{Q}$, and “true” is an emergent property of S^3 , etc.

Given such sequence $\{\text{Int}^i\}_{i=0}^n$ we can define a code of degree k as a consecutive string of the total code which has the property of Obs^k , i.e. if the code can produce an output that is an emergent property of S^k .

We can then view the final code of degree n , Code_n , as a composition of sub-codes of degree $n-1$, Code_{n-1}^i , etc.

Note that Baas indicates this application in mentioning the word *hyperalgorithms* on p. 526 in [4].

How can one think of a good implementation of these functions? The choice of the interactions Int will give us a chance to find fine structures. What happens to our example if we start by $\text{Int}^0 = \{+\}$ and then $\text{Int}^1 = \{-\} \cup \text{Int}^0$ etc? Is there a “natural” choice of that interaction sequence for a given case?

5 Some measures

Let us list a couple of measures that would be useful to capture some of the features mentioned in the Section 1 above, and which also utilizes different levels of codes discussed above.

5.1 Spaghetti

Let us propose a kind of “code-madness-measure” using the above hierarchies of codes.

Let m_k be the maximum numbers of Code_{k-1} codes in a Code_k . More precisely, Let

$$\eta_k^i = \max\{j : \text{Code}_{k-1}^{i,j} \subset \text{Code}_k^i\},$$

and let

$$m_k = \max_i \eta_k^i \text{ and } s_k = \sum_i \eta_k^i.$$

Now, we define the “spaghetti length” at level k to be

$$S_k(\text{Code}_n) = \frac{m_k}{s_k} \text{ and}$$

$$S(\text{Code}_n) = \max_k S_k(\text{Code}_n).$$

5.2 Reuse

Let $0 < k \leq n$

$$R_k^i(\text{Code}_n) =$$

$$\frac{\max \# \text{Code}_{k-1} \subset \text{Code}_k \text{ used } i \text{ times or more}}{s_k}.$$

Let us use the conventions $R_k^2(\text{Code}) = R_k(\text{Code})$ and $R_2^i(\text{Code}) = R^i(\text{Code})$.

5.3 Redundancy

A very important feature in evolutionary driven codes are their robustness. There are good measures of robustness given in the literature. One way to measure it is to check the probability that the code “survives” a one point mutation.

The redundancy in a code of degree k , could be measured in the following way.

Let m be the maximal number of subunit codes of type Code_{k-1} in the code of type Code_k , that can be taken away without affecting the output of the Code_k code, and let n be the total number of subunits. Let us then define the redundancy in code C of type Code_k by

$$\text{Red}(C) = \frac{m}{n}.$$

5.4 Brittleness

Another function that might be better to use in some ways would be a “brittleness” function that we define in the following way.

Let m and n be as above and let $d(k)$ be the number of Code_{k-1} codes in a Code_k code, that when removed

totally, or partially, destroys the code Code_k . The we define the brittleness of Code_k as.

$$\text{Britt}(\text{Code}_k) = \frac{d(k)}{n - m}.$$

That can be viewed in the following way. Let us think of Code_k as a chain and the subunits as links in that chain. Then the length of the chain will be $n - m$ and $d(k)$ will be the number of links that are can not be removed without breaking the chain.

Note also that in the special case when we either have one or two links for each step in the chain, that $d(k) = n - 2m$.

Note that the probability to survive a deletion of a randomly chosen subcode is $1 - d(k)/n$. That is, if there would just be one sublevel to the code, $1 - d(k)/n$ would be the usual robustness measure mentioned above.

6 Five applications

Since we are mainly interested in searching for a evolutionary universal coding style, we are of course interested in the two special cases when the code is a computer code, and when it is a sequence of the DNA. We have tried to make the above definitions of codes and style general enough to be able to deal with those cases.

As a by-product, we noted that this theoretical framework could also be applied to other areas where ‘style’ is essential. The applications that comes closes to our mind was art, music and literature. As a third application we will comment how the above stylistic fingerprint could be used for a common framework in “stylometry” in the study of authorship attribution. Our hope is that if a theory is not only applicable to the special cases it was aimed for under its construction, but also to a different case, it might be a sound approach in that theory.

A fourth possible application would be a stylistic investigation of the internal architecture of black boxes in the theory of neural nets, and its carbon based version—the brain.

The fifth application is about artificial life. We will make a small experiment in such an environment.

6.1 Computer code

By looking at the indicated toy-example above where we had natural numbers as inputs and $+$, $-$ as the first interactions, it is not to hard to imagine that you would get the intuitive “usual meaning” increase in complexity in substructures in the code from lower

order arithmetic operations, more complex functions, subroutines, program parts, the complete program.

Note that what usually is seen as a good programming style, that is separate codes into small, more or less, independent units, and not too many jumps back and forth, will give you a low $S(\text{Code})$; see Section 5.1.

Let us now mention three existing families of computer code measures. See also [10] and [12] for a detailed description of the two first examples and many others.

6.1.1 Halstead’s Complexity Measures

In 1977 M. Halstead introduced a tool to measure the complexity of a computer program. It is perhaps the most well known measure of that kind.

The measure, or more precisely the family of five measures, is based directly on the code in the following way. Let n_1 be the number of distinct operators, n_2 the number of distinct operands, N_1 the total number of operators, and N_2 the total number of operands. From these numbers, the following measures are constructed.

Program vocabulary	$n = n_1 + n_2$.
Program length	$N = N_1 + N_2$.
Difficulty	$D = \frac{n_1 N_2}{2n_2}$.
Volume	$V = N \log_2(n)$.
Effort	$E = DV$.

The Halstead’s measure seems to be a good candidate for measures in the stylistic search since it is only based on textual information and due to the fact that it has been used in many contexts and over such a long time and hence its properties are quite well known.

6.1.2 McCabe’s Cyclomatic Complexity

In 1976, T. McCabe introduced a measure of the number of linearly independent paths through a computer program as a measure of the complexity of the code.

The cyclomatic complexity, CC , is computed in the following way. Let us study a schematic graph of the program and count the number of edges E , the number of nodes N , and the number of connected components c . Then

$$CC = E - N + c.$$

If a program has a CC higher than 50 it is said to be unstable, since it is then “very likely” break down if it is altered.

The Cyclomatic Complexity is more of a measure of the inner logical complexity than the textual Halstead's measure.

6.1.3 GRASP

Let us describe an ongoing project at Auburn, Alabama, which address a numerical local measure of computer codes, and its display. See [9] for further information and down-loading of the program.

“The overall goal of the GRASP project is to improve the comprehensibility of software. Thus, it is important to be able to identify complex areas of source code. The Complexity Profile Graph (CPG), a new graphical representation based on a composite of statement level complexity metrics provides the user with the capability to quickly recognize complex areas of source code. The CPG is significant in that it shows the complexity of a program unit as a profile of statement level complexity metrics rather than as a single, global metric.”

First the program code is parsed into non overlapping segments; then a series of measures, briefly described below, is applied to each segment, giving a local complexity measure of the program code.

The content complexity of a segment S in the code is defined as

$$\eta(S) = \log\left(\sum_{T \in S} \text{Weight}(T)\right),$$

where T are tokens in the segment S . For example, in [9], the weights for Ada 95 are given in the table below.

Token Description	Symbol	Weight
Logical operators	and, or, not, ...	1.5
Comparison op.	<, >, =, <=, ...	1.5
Left parenthesis	(1.3
Identifiers	var1, proc1, ...	1.0
Others	+, -, *, /,), ...	1.0

“The context complexity provides a baseline level of complexity for segments of simple statements nested within a compound statement, which itself may be nested several levels deep. The complexity of a compound statement is based on three aspects: inherent complexity, reachability, and breadth.”

These three complexities are added, with weights, to obtain the context complexity.

Combining the content complexity and the context complexity, by a weighted sum, gives the profile metric $\mu(S)$ for a segment S .

The local metric μ can then be graphically presented as a histogram to give indications where the code is more complex. Thus that would help a programmer to point out code segments that would need some extra thought.

6.1.4 Finding a coding style

Suppose that we would like to find a way to assign a specific style to a programmer. How could we do that?

Suppose he writes in C++. Then one might take a sample of his codes, look at his functions and sub-routines. Go to other programmers and find as many functions as possible from that environment that one would like to be able to identify “our” programmer in the future.

Sort the codes into function classes \mathcal{C}_f where our programmer has written $a_f \in \mathcal{C}_f$ and other programmers $b_{f,j} \in B \subset \mathcal{C}_f$.

Let us now take a wide variety of measures of computer codes, such as those mentioned above, e.g. Halstead's measures etc. Let us call the vector of those measures μ , where each μ_i is a function of a C++ code to the unit interval $[0, 1]$.

Let use equation (1).

$$\mathbf{u} = \sum_f \sum_{b_{f,j} \in B} (\mu(a_f) - \mu(b_{f,j})).$$

Now,

$$\mathbf{w}^+ = \frac{\mathbf{u}}{\|\mathbf{u}\|}$$

will be the stylistic fingerprint of this programmer with respect to the vector of measures μ and in the chosen environment. Note that \mathbf{w}^+ will be heavily dependent on the chosen reference codes, so it is important that that environment is chosen carefully.

6.2 DNA

It is hard to get a handle on the DNA code with usual computer code tools. As an example in [17] the authors study *block entropies* for DNA to find some indication of structure.

Definition 6.1 *Let the length of the alphabet be λ . Then the (normalized) n -block entropy of a sequence is defined as*

$$H_n = - \sum_{i=1}^{\lambda^n} p_i^{(n)} \log_{\lambda} p_i^{(n)},$$

where $p_i^{(n)}$ is the probability of the i th combination of n “letters”.

In the summary of [17] one can read the following.

“Surprisingly, DNA sequences behave closer to completely random sequences than to written text. The very strict syntax of computer languages on the other hand is reflected by a very low average information content of its sub-strings.”

To us that means that the style of DNA sequences is not just close to chaos, but rather written in such a different style compared to written text, and even more different from computer codes.

The inputs, S^0 here are the amino acids, and one could take perhaps Int^0 to be “putting next to”, or sequencing.

The letters on the DNA level should be the four bases, the words are then three letters word coding for a amino acid. Add to the dictionary special start and stop words for the genes.

One could also study the situation on the amino acid level, i.e. one level up from the bare DNA code. That would give us 20 letters in an alphabet.⁴ The words would here be the genes.

6.2.1 Hopes

One would hope that some hypothetical insight of a universal evolutionary driven style would give some hints how to better “read” the DNA code.

We would therefore try to find measures that are general enough in the below described computer experiment, so that some hypothesis about the DNA code could eventually be made.

There are indications that evolutionary driven code, may not be “optimal” in a basic sense, but might include peculiar turns and twists. See for example p. 180 in [11] where J. Madox discuss *RNA Editing*

“The puzzle is to know why these changes, which are presumably advantageous to the organism, have not been incorporated in the gene themselves, thus avoiding the need for editing by way of afterthought—not to mention the need for a separate biochemical mechanism for carrying it out.”

He also addresses, on p. 203, the “junk code” in eukaryotic cells.

⁴The alphabet is not unique, e.g. different spelling in example some bacterias and humans for some amino acids.

“At the very least, this complication is an extra metabolic cost for eukaryotic cells. It is also potentially a source of error. What countervailing selective advantage can there possibly be in this arrangement?”

6.3 Literature

Let us now turn our attention to something different. Let us look at some examples in literature where “style” has been in the focus.

On p. 74 in [14] the author discuss computational differences between grammatical errors and stylistic weaknesses.

In [15], seven important problems with the existing authorship attribution studies are listed and discussed and some solutions proposed. The proposed solution to problem number three is to

“study style in its totality. Approximately 1,000 style markers have already been isolated. We must strive to identify all of the markers that make up “style” — to map style the way biologists are mapping the genes.”

Furthermore, the suggested solution to problem five is to

“Develop a complete and necessarily multi-faceted theoretical framework on which to hang all non-traditional authorship attribution studies.

Publish the theories, discuss the theories, and put the theories to experimental tests.”

As an example of a suggested metric from the literature studies, one can take the Yule’s coefficient advocated among many others in [5]. Let $\{f_{ij}\}$ represent the observed frequencies in a “two way contingency table” and let the Yule’s coefficient (see [20]) be defined as

$$Y = \frac{\sqrt{c-1}}{\sqrt{c+1}}, \text{ where } c = \frac{f_{11}f_{22}}{f_{12}f_{21}}.$$

6.3.1 Stylometry: Finding the author

Let us now treat a hypothetical case, using the methods from Section 3, on the authorship attribution problem.

What do we mean by a code in this case? Let us look at Definition 2.1. We will interpret the “letters” as word taken from the “alphabet” which will

in this case be a complete dictionary of the language in question. What about the functions?

Scarry gives in [16] a description how we can think about the reading process; see the following quote from the first chapter:

“When we say ‘Emily Brontë describes Catherine’s face,’ we might also say ‘Brontë gives us a set of instructions for how to imagine or construct Catherine’s face.’ This reformulation is accurate if cumbersome, in that it shifts the site of mimesis from the object to the mental act.”

So, in this case we might think about the functions as descriptions, or simply constant functions, where the interpreter is the reader.⁵ Examples of interpreted functions would be text where “boy meets girl”, or “prince meets ghost”. An even more refined version would be “boy meets girl described in an English sonnet”.

Suppose now that we want to test the hypothesis that author X has written a given sonnet s . Then we might gather all known sonnets written by X into the set A as a subset of reference sonnets from that time period in S . Now $a_i \in A$ means sonnet number i in A .

One wants to have as large environment S as possible, but at the same time also as narrow as possible, i.e. from the same time period, etc. This has then to be chosen carefully and with great knowledge about the literature period and its authors. Let now B be the set of comparison sonnets.

On the other hand when it comes to choose metrics, then we pick as many as it is numerically computable in reasonable time, which depends both on our time and our computer. For example, there has been some new interesting development using neural networks in authorship attributions, see for example [19]. An even more exciting method was used in [8] where they used genetic algorithms in order to find the best features to measure. We can use such nets and genetically derived measures in our set of measures too!

Now, apply equation (1) to get the vector \mathbf{u} which then is normalized to \mathbf{w}^+ . That will be the stylistic finger print of author X , given the above constructed framework.

How good and reliable is this fingerprint? Suppose that A is large and S is rich, not only large but more

or less complete with respect to the author representation. Then η from equation (4) would be a good measure how reliable \mathbf{w}^+ is. We want η to be large of course, but what is large enough?

To answer that we need to study the actual distributions of the sonnets evaluated by $\nu_{\mathbf{w}}$, make approximations and perform hypothesis tests.

The nice thing about this method is that one does not have to argue which measure should be applied. Just apply them all!

Talking about measures, there has been a very animated debate about the values of using computers in literary studies. R. Quiones said in [6] “Why don’t they simply read the plays?”. A literature expert reading a text is undoubtedly very hard to beat when it comes to authorship attributions. But let us look at this situation having our suggested definition of measures of codes in mind. Isn’t the expert using a long array of measures, weighted together in an intricate and sometimes subconscious way? One measure could be: “ X would never use that word in two consecutive sentences”. The measure would be the characteristic function of that event in the text, and the weight would be heavily negative. The more skill and familiarity the expert has about such tasks, the larger the array μ , and the more subtle the weighing process would be. It may seem like a trivialization to think in those terms, but since the task is very hard and complex, one would not expect that a computer would be programmed in the near future that would be generally better than a literature expert. Compare with the relatively straightforward problem to play chess.

6.4 Neural nets

P. Adams in [2] pointed out the possibility of strong evolutionary forces acting inside the brain in the process of learning. “Good” synapses will be rewarded by being strengthened, and “bad” will be punished by being weakened. What is good and bad are much more intricate and implicit qualities compared to the genetic evolution, but maybe evolutionary forces are in command in the learning process on a time scale of seconds instead of millenias. And if there is a universal coding style—that should then be found in the style of the programming of the neural nets too.

6.5 Artificial life

Avida, see [3] and [1], is a program in the Tierra class, see [18]. Unlike Tierra it gives a natural 2 dimensional picture of an evolutionary process. Like Tierra, Avida is *not* a simulation of real carbon based

⁵Here it is easy to see the crucial importance of the interpreter. I would for example be an extremely poor interpreter of a French text, even if I would get some picture of a story at the end.

DNA, but a real evolution in a silicon based (simple) world. We will now do an experiment in the Avida world.

7 A small experiment

Let us try some of the above concepts in a Avida experiment. We will deliberately try to make it as simple as possible in order to get some output in a straightforward way. But we will keep all the doors open to make variants and generalizations in the future.

We use Avida version 1.0.1 that is available on the web; see [3].

When running the program, you have the possibility to extract individuals and saving their data and their genetic code. To read more about this, see the documentation on [3] or even better—the book [1]. The code and the data is saved to files such as `153-aagxs`.

The data in `153-aagxs` tells you, for example, that in addition to being able to replicate itself, the code also performs some other tasks. In this specific case, it takes input from a stack, performs a logical XOR twice, performs three NOTs, etc. For this, it is rewarded with a bigger time slice, and hence will reproduce (and survive) better.

7.1 The function class

Let us as the function f defining the code universe \mathcal{C}_f , take a function that exactly performs the above described set of tasks, e.g. three NOTS etc.

As the subspace A we simply take the generated avida code in `153-aagxs`.

7.2 Comparison codes

To get a comparison environment, let us construct (or simulate) two, man-made codes that perform the operations in f .

We use a very simple approach and simulate two different codes in B . One with no loop, except for the self-copying loop, and one with as many loops as there are logical tasks to be done. Furthermore, we don't actually write the codes but simulate the writing using a very rigid approach of making all the logical statements from combinations of NANDs⁶, and then in detail study the needed operations just in one NAND.

⁶This is the base for the default reward list for completed tasks in time slicing; see the file `task.set` in the Avida package.

This approach will give us a list of operations, and operands needed to fulfill f . We can now try to look for style.

7.3 The measure

To start with something, we used the Halstead's measures as our μ . That is, let

$$\mu = (\text{vocabulary, length, difficulty, volume, effort}).$$

7.4 Simulations

The actual simulations is done by extracting creatures, i.e. individual programs, from a run of the Avida program, as described above. The extraction consists of some data, the table of performance, but also the program itself. We then use a C++ program to automatically analyze the extraction by first reading of the data and the performance table, and then find the Halstead's measure vector μ for the actual code. The C++ program then also uses the performance table to simulate the two different comparison codes described in Section 7.2 above and to calculate their Halstead's measures respectively. The program then also computes \mathbf{w} when A has only the code of extracted individual, and B consist of the two comparison codes. (\mathbf{w} for other combinations of A and B are also considered.) The results are then exported to a Maple file where one can more easily work with the output.

7.5 Preliminary results

Since $\#A$ is one, and $\#B$ is two, we can not talk about results in any statistical sense of course. Nevertheless, we can present some outcome that should be seen as a indicator of what eventually can be done. Even if we have a very small \mathcal{C}_f , since essentially every creature represents a unique list of performed tasks, which leads to essentially a unique function f ; we have many classes \mathcal{C}_f , and we are free to change parameters, such as the initial random seed, the reward table for the tasks, etc. We can therefore compare profiles; see for example Figure 2.

Let us more in detail see what kind of output you can get by going back to our old friend, born after 19441 generations, `153-aagxs`.

After feeding the file `153-aagxs` into the C++ program, which dissects the code, and simulates the two comparison codes, we get as outputs things like: The Halstead's measures:

$$n_1 = 19, n_2 = 3, N_1 = 153, N_2 = 31$$

difficulty = 98.1667

volume = 820.535

effort = 80549.2.

And we also get

$\theta = 0.0085549$ and $\eta = 391865$,

which does not really tell you much in this meager situation (η is huge since the variance of X is so extremely tiny for this special case). We can view \mathbf{w}^+ in a diagram; see Figure 3. (Remember that we normalized the measures into $[0, 1]$ by the transformation $\frac{x}{1+x}$ in order to make the weights in \mathbf{w} play in the same division.)

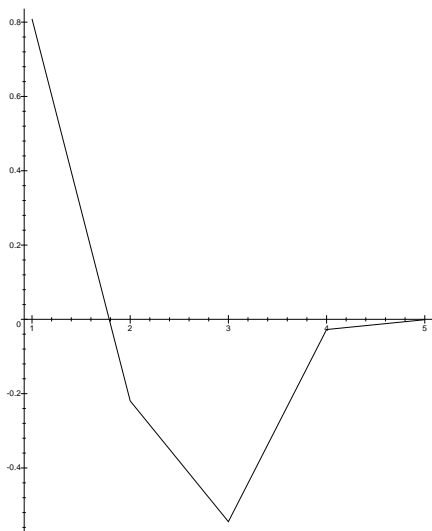


Figure 1: *Here is an example of a fingerprint after about 1000 generations using Halstead's complexity measures as μ .*

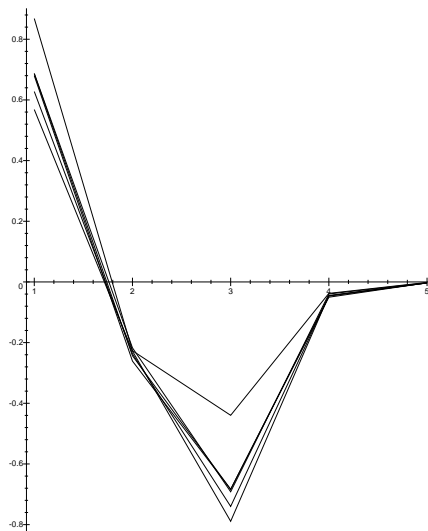


Figure 2: *Here are seven fingerprints after about 8500. Can we hope for some convergence? And if so, what will that tell us?*

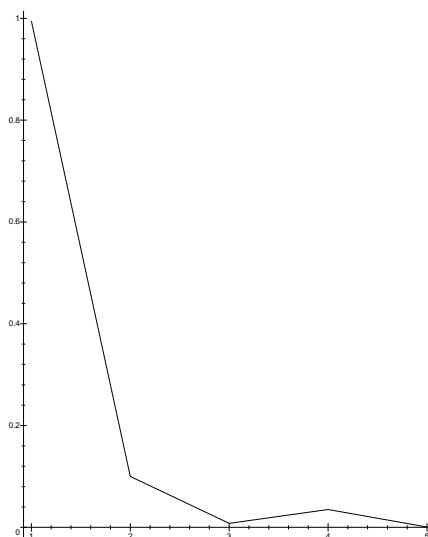


Figure 3: *Here is \mathbf{w}^+ when A is the single Avida generated code 153-aagxs and B consists of the no-loop-code and the all-loop-code, both based entirely on NAND combinations.*

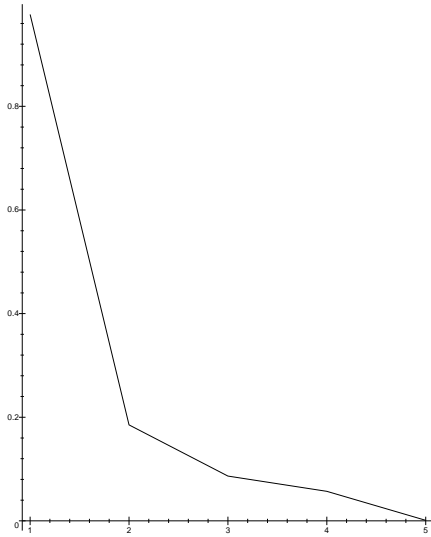


Figure 4: \mathbf{w}^+ when A is 153-aagxs and B is the single no-loop-code.

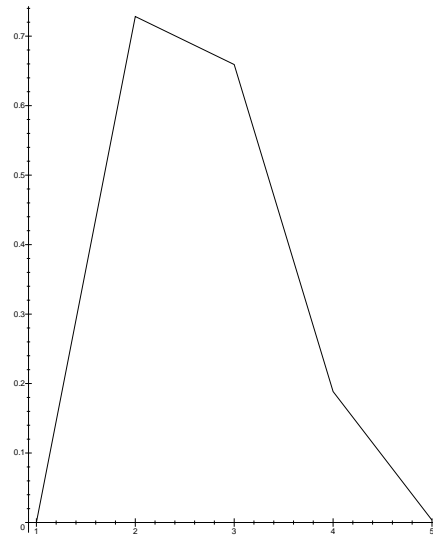


Figure 6: \mathbf{w}^+ when A is the all-loop-code and B is the no-loop-code.

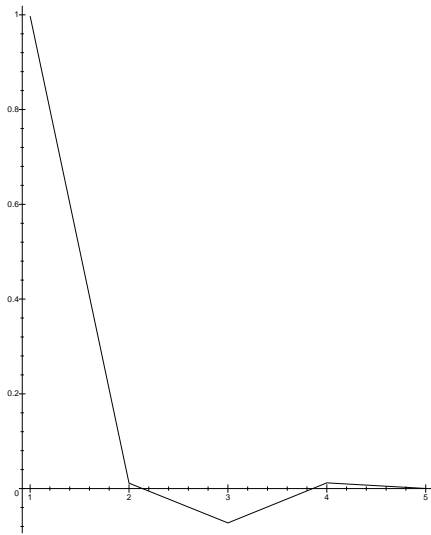


Figure 5: Here is A 153-aagxs and B is the all-loop-code.

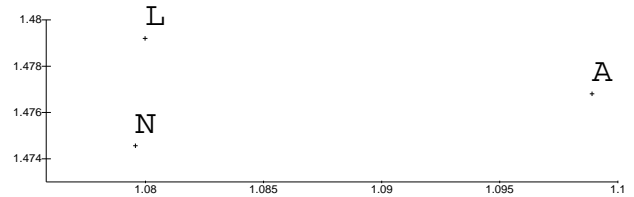


Figure 7: Here is a picture of a principal component analysis, see Section 3.6 of the μ vector for the three different codes connected to 153-aagxs. The letter A stands for the Avida code and the letters N and L for the no-loop code and the loop code. We see that the two simulated codes, N and L , are more together indicating that they are more similar to each other than the evolutionary generated code from Avida.

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